

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/684,149A
Source: 1FW/6
Date Processed by STIC: 1/9/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/09/2007

PATENT APPLICATION: US/10/684,149A

TIME: 13:11:43

Input Set : N:\efs\01_09_07\10684149a_efs\02-17AMENDEDSEQUENCE.TXT

Output Set: N:\CRF4\01092007\J684149A.raw

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4 <110> APPLICANT: West, James W.
5      Brandt, Cameron S.
6      Jaspers, Stephen R.
8 <120> TITLE OF INVENTION: Production of Homotrimeric Fusion
9      Proteins
11 <130> FILE REFERENCE: 02-17
13 <140> CURRENT APPLICATION NUMBER: 10/684,149A
14 <141> CURRENT FILING DATE: 2003-10-10
16 <150> PRIOR APPLICATION NUMBER: 60/417,801
17 <151> PRIOR FILING DATE: 2002-10-11
19 <160> NUMBER OF SEQ ID NOS: 23
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 10
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: C-myc tag
31 <400> SEQUENCE: 1
32 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
33 1          5          10
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 9
38 <212> TYPE: PRT
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Hemagglutinin A epitope tag
44 <400> SEQUENCE: 2
45 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
46 1          5
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 1377
51 <212> TYPE: DNA
52 <213> ORGANISM: Human
54 <220> FEATURE:
55 <221> NAME/KEY: CDS
56 <222> LOCATION: (14)...(892)
58 <400> SEQUENCE: 3
59 agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg      49
60      Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
61      1          5          10
63 agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg      97
64 Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly

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65	15	20	25	
67	gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg	145		
68	Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu			
69	30 35 40			
71	ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc	193		
72	Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg			
73	45 50 55 60			
75	acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc	241		
76	Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly			
77	65 70 75			
79	aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc	289		
80	Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile			
81	80 85 90			
83	tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc	337		
84	Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu			
85	95 100 105			
87	agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga	385		
88	Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly			
89	110 115 120			
91	gaa gtt gaa aac aat tca gac aac tgc gga agg tac caa gga ttg gag	433		
92	Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu			
93	125 130 135 140			
95	cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt	481		
96	His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser			
97	145 150 155			
99	gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt	529		
100	Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys			
101	160 165 170			
103	gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag	577		
104	Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys			
105	175 180 185			
107	agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt	625		
108	Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser			
109	190 195 200			
111	ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg	673		
112	Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val			
113	205 210 215 220			
115	agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag	721		
116	Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu			
117	225 230 235			
119	tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac	769		
120	Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp			
121	240 245 250			
123	ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg	817		
124	Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu			
125	255 260 265			
127	cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg	865		
128	Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val			
129	270 275 280			

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131 cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg          912
132 Pro Ala Gln Glu Gly Gly Pro Gly Ala
133 285                290
135 aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972
136 gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032
137 gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092
138 ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152
139 ggggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggaggtc 1212
140 ggggcactct gagtcccagt tcccagtgca gctgtaggtc gtcacacct aaccacacgt 1272
141 gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctcctc ctggagaata 1332
142 aaaccttttg cagctgccct tcctcaaaaa aaaaaaaaaa aaaaa          1377
144 <210> SEQ ID NO: 4
145 <211> LENGTH: 293
146 <212> TYPE: PRT
147 <213> ORGANISM: Human
149 <400> SEQUENCE: 4
150 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
151 1          5          10          15
152 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
153 20          25          30
154 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
155 35          40          45
156 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
157 50          55          60
158 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
159 65          70          75          80
160 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
161 85          90          95
162 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
163 100         105         110
164 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
165 115         120         125
166 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
167 130         135         140
168 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
169 145         150         155         160
170 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
171 165         170         175
172 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
173 180         185         190
174 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
175 195         200         205
176 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
177 210         215         220
178 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
179 225         230         235         240
180 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
181 245         250         255
182 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro

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183          260          265          270
184 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
185          275          280          285
186 Gly Gly Pro Gly Ala
187          290
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 21
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: PCR primer
198 <400> SEQUENCE: 5
199 gggcctccag gccaccagg t                               21
201 <210> SEQ ID NO: 6
202 <211> LENGTH: 21
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: PCR primer
209 <400> SEQUENCE: 6
210 tcacattgga gccactagga a                               21
212 <210> SEQ ID NO: 7
213 <211> LENGTH: 56
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: PCR primer
220 <400> SEQUENCE: 7
221 acaggtgtcc aggggaattca tataggccgg ccaccatgga tgcaatgaag agaggg 56
223 <210> SEQ ID NO: 8
224 <211> LENGTH: 36
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: PCR primer
231 <400> SEQUENCE: 8
232 accctcaggc atcgaacccg aaccggaacc ggatcc             36
234 <210> SEQ ID NO: 9
235 <211> LENGTH: 118
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR primer
242 <400> SEQUENCE: 9
243 gatcggatcc atggccgaaa ctgatacctaa aacagttcaa gaccttacca gcgtagtcca 60
244 gacgctcctg caagagatcg aagataagtt tcagactatg agcgaccaaa tcattgag 118
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 100
248 <212> TYPE: DNA

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249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: PCR primer
254 <400> SEQUENCE: 10
255 agaatgcatg acatgagctc caggatagat gaccttgaga aaaatatagc agatttaatg 60
256 acgcaagctg gtgtggaaga gttggaagga agtggttcta 100
258 <210> SEQ ID NO: 11
259 <211> LENGTH: 110
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: PCR primer
266 <400> SEQUENCE: 11
267 gatctagaac cacttccttc caactcttcc acaccagctt gcgtcattaa atctgctata 60
268 tttttctcaa ggtcatctat cctggagctc atgtcatcga ttctctcaat 110
270 <210> SEQ ID NO: 12
271 <211> LENGTH: 108
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: PCR primer
278 <400> SEQUENCE: 12
279 gatttggtcg ctcatagtct gaaacttatt ttgcatctct tgcaggagcg tctggactac 60
280 gctggtaagg tcttgaactg ttttaggatc agtttcggcc atggatcc 108
282 <210> SEQ ID NO: 13
283 <211> LENGTH: 33
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: PCR primer
290 <400> SEQUENCE: 13
291 cacacgtacg aagatggatg caatgaagag agg 33
293 <210> SEQ ID NO: 14
294 <211> LENGTH: 30
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: PCR primer
301 <400> SEQUENCE: 14
302 ggtagatct cgaacccgaa cccgaaccgg 30
304 <210> SEQ ID NO: 15
305 <211> LENGTH: 62
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: PCR primer
312 <400> SEQUENCE: 15
313 ctagaaataa ttttgtttaa ctttaagaag gagatatata tatggctatg agatcctgcc 60
314 cc 62

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VERIFICATION SUMMARY

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Input Set : N:\efs\01_09_07\10684149a_efs\02-17AMENDEDSEQUENCE.TXT

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